

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 19, 2002, 14:53:27 : Search time 22 Seconds
(without alignments)
2482.016 Million cell updates/sec

Title: US-08-813-323b-2

Perfect score: 3008

Sequence: 1 MESSKKMDSFGALQTNPPK.....IKDDTIFKVIYDTSPLPP 568

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3008	100.0	568	2	A55960 CD40 receptor-asso
2	2886.5	96.0	567	2	I49272 CD40 receptor-asso
3	2839.5	94.4	543	2	S68467 CD40 receptor-asso
4	1192.5	39.6	557	2	JC6539 tumor necrosis fac
5	837.5	27.8	501	2	T61512 TNF receptor assoc
6	811	27.0	501	2	S56163 tumor necrosis fac
7	636.5	21.2	416	2	B55649 TNF-associated pr
8	628	20.9	409	2	A54750 TNF receptor assoc
9	560.5	18.6	470	2	I38026 MLN 62 protein - h
10	552	18.4	522	2	S71821 probable interleuk
11	522.5	17.4	509	2	T22338 hypothetical prote
12	201	6.7	458	2	A29361 DG17 protein - sll
13	173.5	5.8	313	2	B96692 hypothetical prote
14	159	5.3	634	2	I49642 nuclear phosphopro
15	152.5	5.1	609	2	A43906 meprin A (EC 3.4.2
16	151.5	5.0	704	2	A48040 CGI protein - huma
17	150.5	5.0	1300	2	I53799 hypothetical prote
18	150	5.0	1005	2	A64465 hypothetical prote
19	149.5	5.0	919	2	B72765 hypothetical prote
20	148.5	4.9	1085	2	F96712 hypothetical prote
21	148	4.9	1676	2	E71410 probable centromer
22	148	4.9	1957	2	T38077 hypothetical colle
23	147.5	4.9	1356	2	S32763 kinectin 1 - human
24	146	4.9	1039	2	S18199 myosin heavy chain
25	145.5	4.8	1218	2	T14265 golgin-245 - mouse
26	145.5	4.8	1577	2	T19722 hypothetical prote
27	145	4.8	1679	2	S48385 hypothetical prote
28	144.5	4.8	1104	2	I38869 transcription fact
29	144	4.8	1727	2	T50073 myosin-like coiled

30	143.5	4.8	852	2	D72230 conserved hypothet
31	143	4.8	698	2	S52696 myosin heavy chain
32	142.5	4.7	1313	2	P66673 hypothetical prote
33	142	4.7	2253	2	I30336 nuclear/mitotic ap
34	141.5	4.7	412	2	D88072 protein ZK1240.1
35	141.5	4.7	1690	2	T13030 microtubule bindin
36	141	4.7	879	2	C71083 conserved hypothet
37	141	4.7	1046	2	A66790 ATP-dependent dsDN
38	141	4.7	1940	1	A24922 myosin heavy chain
39	139.5	4.6	512	2	F66193 hypothetical prote
40	139.5	4.6	631	2	UC4298 hyaluronan recepto
41	139.5	4.6	1164	2	T24806 hypothetical prote
42	139	4.6	551	2	JC7562 glioblastoma RING
43	138	4.6	1187	2	T18355 hypothetical prote
44	137.5	4.6	1607	2	T43212 insulin-like growt
45	137	4.6	886	2	H63378 conserved hypothet

ALIGNMENTS

RESULT 1

A55960
CD40 receptor-associated factor 1 - human
N:Alternate names: CD40-binding protein
C:Species: Homo sapiens (man)
C>Date: 15-Mar-1996 #sequence, revision 15-Mar-1996 #text, change 01-Dec-2000
C:Accession: A55960; A55649; A55135
R:Cheng, G.; Cleary, A.M.; Ye, Z.S.; Hong, D.I.; Lederman, S.; Baltimore, D.
Science 267, 1494-1498, 1995
A:Title: Involvement of CRAF1, a relative of TRAF, in CD40 signaling.
A:Reference number: A55960; MUID:95184010; PMID:7533327
A:Accession: A55960
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-568 <RES>
A:Cross-references: EMBL:021092; NID:9726087; PIDN:AA50112.1; PID:9726088
R:Mosialos, G.; Birkenbach, M.; Yalamanchili, R.; VandeSalle, T.; Ware, C.; Kieff, E.
Cell 80, 389-399, 1995
A:Title: The Epstein-Barr virus transforming protein Lmp1 engages signaling proteins
A:Reference number: A55649; MUID:95163092; PMID:7859281
A:Accession: A55649
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-128, 'W', 130-568 <MOS>
A:Cross-references: GB:019260; NID:9675459; PIDN:AA65732.1; PID:9675460
R:Hu, H.M.; O'Rourke, K.; Boguski, M.S.; Dixit, V.M.
J. Biol. Chem. 269, 30069-30072, 1994
A:Title: A novel RING finger protein interacts with the cytoplasmic domain of CD40.
A:Reference number: A55135; MUID:95073988; PMID:7527023
A:Accession: A55135
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-128, 'W', 130-133, 135-404, 'G', 406-568 <HUA>
A:Cross-references: GB:015637; NID:9595910; PIDN:AA56753.1; PID:9595911
C:Gene: CRAF1
C:Superfamily: CD40 receptor-associated protein GAP-1; RING finger homology
C:Keywords: coiled coil; zinc
F:49-97/Domain: RING finger homology <RING>

Query Match 100.0%; Score 3008; DB 2; Length 568;
Best Local Similarity 100.0%; Pred. No. 9, 6e-167;
Matches 568; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MESSKKMDSFGALQTNPPKLTHTDSAGTPYFVPOGGKKEFKYTVEDKCKCKCHLV 60
DB 1 MESSKKMDSFGALQTNPPKLTHTDSAGTPYFVPOGGKKEFKYTVEDKCKCKCHLV 60
QY 61 CSPKTEGCHRFECESCMALLSSSPKCTACQESIVKDKVKNCKCKREILALDIYCRNE 120
DB 61 CSPKTEGCHRFECESCMALLSSSPKCTACQESIVKDKVKNCKCKREILALDIYCRNE 120

QY 121 SRGCAEQLTLGLHLVHLKNDCHFEELPCVPRDCKEKLKRDLDHVEKACKYREATCSHC 180
 |||||
 Db 121 SRGCAEQLTLGLHLVHLKNDCHFEELPCVPRDCKEKLKRDLDHVEKACKYREATCSHC 180
 QY 181 KSOVPMIALOKHEDTDCPCVVVSCPHKCSVOYTLRLSELSEHLSECVNAPSTCSFKRYGCV 240
 |||||
 Db 181 KSOVPMIALOKHEDTDCPCVVVSCPHKCSVOYTLRLSELSEHLSECVNAPSTCSFKRYGCV 240
 QY 241 FOGTNOQIKAHESASAVOHVNLKEMNSLEKRVSLLONESVEKNKSIOSLHNOICSEFI 300
 |||||
 Db 241 FOGTNOQIKAHESASAVOHVNLKEMNSLEKRVSLLONESVEKNKSIOSLHNOICSEFI 300
 QY 301 EIEROKEMLRNNESKILHLORVIDSOAEKLELDEIRPFROWNEADSMKSSVESLONR 360
 |||||
 Db 301 EIEROKEMLRNNESKILHLORVIDSOAEKLELDEIRPFROWNEADSMKSSVESLONR 360
 QY 361 VTELESVDKSAGQVARNVTGLLESQLSRHDQMLSVHDIRLADMDLRFVYLETASYNGVLIW 420
 |||||
 Db 361 VTELESVDKSAGQVARNVTGLLESQLSRHDQMLSVHDIRLADMDLRFVYLETASYNGVLIW 420
 QY 421 KIRDYKRRKQEAVMGKTLSTYSQPFYTGFGYKMCARVYLNGDMGKGTSLFFVIMRG 480
 |||||
 Db 421 KIRDYKRRKQEAVMGKTLSTYSQPFYTGFGYKMCARVYLNGDMGKGTSLFFVIMRG 480
 QY 481 EYDALLPMPFKOKVTLMLMDQSSRRHLGDAFKPDPNSSSEKPKPTGEMNIASGCPVFAQ 540
 |||||
 Db 481 EYDALLPMPFKOKVTLMLMDQSSRRHLGDAFKPDPNSSSEKPKPTGEMNIASGCPVFAQ 540
 QY 541 TVLENGTYIKDDTIFIKVIVDTSDLPDP 568
 |||||
 Db 541 TVLENGTYIKDDTIFIKVIVDTSDLPDP 568

RESULT 2

CD40 receptor-associated factor 1 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 18-Aug-2000
 C:Accession: I49272
 R:Cheng, G.; Cleary, A.M.; Ye, Z.S.; Hong, D.I.; Lederman, S.; Baltimore, D.
 Science 267, 1494-1498, 1995
 A:Title: Involvement of CRAF1, a relative of TRAF, in CD40 signaling.
 A:Reference number: A55960; MUID:95164010; PMID:7533327
 A:Accession: I49272
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-567 <RES>
 A:Cross-references: EMBL:U21050; NID:g719292; PIDN:AAC52175.1; PID:g719293
 C:Genetics:
 A:Gene: CRAF1
 C:Superfamily: CD40 receptor-associated protein CAP-1; RING finger homology
 C:Keywords: zinc finger
 F:48-96/Domain: RING finger homology <RNG>

Query Match 96.0%; Score 2886.5; DB 2; Length 567;
 Best Local Similarity 96.1%; Pred. No. 1e-159;
 Matches 546; Conservative 7; Mismatches 14; Indels 1; Gaps 1;
 QY 1 MESKKMDSGALQTNPPKLHTRDSAGTPVPPDGGYKKEKFTVEDKYKCEKCHLYL 60
 |||||
 Db 1 MESKKMDSGALQTNPPKLHTRDSAGTPVPPDGGYKKEKFTVEDKYKCEKCHLYL 60
 QY 61 CSPKQTECHGRFCESMAALLSSSSPKCTACQESIVKDKYFNCKCKREILALQIYCRNE 120
 |||||
 Db 61 CSPKQTECHGRFCESMAALLSSSSPKCTACQESIVKDKYFNCKCKREILALQIYCRNE 120
 QY 121 SRGCAEQLTLGLHLVHLKNDCHFEELPCVPRDCKEKLKRDLDHVEKACKYREATCSHC 180
 |||||
 Db 121 SRGCAEQLTLGLHLVHLKNDCHFEELPCVPRDCKEKLKRDLDHVEKACKYREATCSHC 180
 QY 181 KSOVPMIALOKHEDTDCPCVVVSCPHKCSVOYTLRLSELSEHLSECVNAPSTCSFKRYGCV 240
 |||||
 Db 181 KSOVPMIALOKHEDTDCPCVVVSCPHKCSVOYTLRLSELSEHLSECVNAPSTCSFKRYGCV 240

QY 241 FOGTNOQIKAHESASAVOHVNLKEMNSLEKRVSLLONESVEKNKSIOSLHNOICSEFI 300
 |||||
 Db 240 FOGTNOQIKAHESASAVOHVNLKEMNSLEKRVSLLONESVEKNKSIOSLHNOICSEFI 299
 QY 301 EIEROKEMLRNNESKILHLORVIDSOAEKLELDEIRPFROWNEADSMKSSVESLONR 360
 |||||
 Db 300 EIEROKEMLRNNESKILHLORVIDSOAEKLELDEIRPFROWNEADSMKSSVESLONR 359
 QY 361 VTELESVDKSAGQVARNVTGLLESQLSRHDQMLSVHDIRLADMDLRFVYLETASYNGVLIW 420
 |||||
 Db 360 VTELESVDKSAGQVARNVTGLLESQLSRHDQMLSVHDIRLADMDLRFVYLETASYNGVLIW 419
 QY 421 KIRDYKRRKQEAVMGKTLSTYSQPFYTGFGYKMCARVYLNGDMGKGTSLFFVIMRG 480
 |||||
 Db 420 KIRDYKRRKQEAVMGKTLSTYSQPFYTGFGYKMCARVYLNGDMGKGTSLFFVIMRG 479
 QY 481 EYDALLPMPFKOKVTLMLMDQSSRRHLGDAFKPDPNSSSEKPKPTGEMNIASGCPVFAQ 540
 |||||
 Db 480 EYDALLPMPFKOKVTLMLMDQSSRRHLGDAFKPDPNSSSEKPKPTGEMNIASGCPVFAQ 539
 QY 541 TVLENGTYIKDDTIFIKVIVDTSDLPDP 568
 |||||
 Db 540 TVLENGTYIKDDTIFIKVIVDTSDLPDP 567

RESULT 3

CD40 receptor-associated protein CAP-1 - human
 C:Species: Homo sapiens (man)
 C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 08-Dec-2000
 C:Accession: S68467; 153498
 R:Sato, T.; Irie, S.; Reed, J.C.
 FEBS Lett. 358, 113-118, 1995
 A:Title: A novel member of the TRAF family of putative signal transducing proteins b1
 A:Reference number: I53498; MUID:95129692; PMID:7530216
 A:Accession: S68467
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-543 <SAT>
 A:Cross-references: EMBL:L38509; NID:g695357; PIDN:AAA68195.1; PID:g695358
 A:Experimental source: t15sue-type fetal brain
 C:Genetics:
 A:Gene: CAP-1
 C:Superfamily: CD40 receptor-associated protein CAP-1; RING finger homology
 C:Keywords: homodimer; signal transduction; zinc finger
 F:49-97/Domain: RING finger homology <RNG>

Query Match 94.4%; Score 2839.5; DB 2; Length 543;
 Best Local Similarity 95.4%; Pred. No. 5.1e-157;
 Matches 542; Conservative 0; Mismatches 1; Indels 25; Gaps 1;
 QY 1 MESKKMDSGALQTNPPKLHTRDSAGTPVPPDGGYKKEKFTVEDKYKCEKCHLYL 60
 |||||
 Db 1 MESKKMDSGALQTNPPKLHTRDSAGTPVPPDGGYKKEKFTVEDKYKCEKCHLYL 60
 QY 61 CSPKQTECHGRFCESMAALLSSSSPKCTACQESIVKDKYFNCKCKREILALQIYCRNE 120
 |||||
 Db 61 CSPKQTECHGRFCESMAALLSSSSPKCTACQESIVKDKYFNCKCKREILALQIYCRNE 120
 QY 121 SRGCAEQLTLGLHLVHLKNDCHFEELPCVPRDCKEKLKRDLDHVEKACKYREATCSHC 180
 |||||
 Db 121 SRGCAEQLTLGLHLVHLKNDCHFEELPCVPRDCKEKLKRDLDHVEKACKYREATCSHC 180
 QY 181 KSOVPMIALOKHEDTDCPCVVVSCPHKCSVOYTLRLSELSEHLSECVNAPSTCSFKRYGCV 240
 |||||
 Db 181 KSOVPMIALOKHEDTDCPCVVVSCPHKCSVOYTLRLSELSEHLSECVNAPSTCSFKRYGCV 240
 QY 241 FOGTNOQIKAHESASAVOHVNLKEMNSLEKRVSLLONESVEKNKSIOSLHNOICSEFI 300
 |||||
 Db 218 --GTNOQIKAHESASAVOHVNLKEMNSLEKRVSLLONESVEKNKSIOSLHNOICSEFI 275
 QY 301 EIEROKEMLRNNESKILHLORVIDSOAEKLELDEIRPFROWNEADSMKSSVESLONR 360

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Db 276 EIERKEMLRNNESKTLHLQVHDSQAEKLELDEKELRSFQNNBEADSMKSSVESLQNR 335
      |||
Oy 361 VTELESVDKSGAVARNTGLLESQLSRHDQMLSVHDIRLADMDLRFVLETAHYNGVLTW 420
      |||
Db 336 VTELESVDKSGAVARNTGLLESQLSRHDQMLSVHDIRLADMDLRFVLETAHYNGVLTW 395
      |||
Oy 421 KIRDYKRRKQEAVMGKTLSTLSQPPYTGFGYKMCARVYLLGDGKGKTHLSFEFVIRG 480
      |||
Db 396 KIRDYKRRKQEAVMGKTLSTLSQPPYTGFGYKMCARVYLLGDGKGKTHLSFEFVIRG 455
      |||
Oy 481 EVDALLPMPFKQKVTLMMDQSSRRHLGDAFPDPPNSSFFKPTGEMNIAAGCPVEVAQ 540
      |||
Db 456 EVDALLPMPFKQKVTLMMDQSSRRHLGDAFPDPPNSSFFKPTGEMNIAAGCPVEVAQ 515
      |||
Oy 541 TVLENGTYIKDDTIFIKVYVDTSLDLP 568
      |||
Db 516 TVLENGTYIKDDTIFIKVYVDTSLDLP 543
      |||

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RESULT 4

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Jc6539
tumor necrosis factor receptor-associated factor 5 homolog - human
C:Species: Homo sapiens (man)
C>Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 18-Aug-2000
C:Accession: Jc6539
R:Mizushima, S.; Fujita, M.; Ishida, T.; Azuma, S.; Kato, K.; Hirai, M.; Otsuka, M.; Yan
Gene 207, 135-140, 1998
A:Title: Cloning and characterization of a cDNA encoding the human homolog of tumor necr
A:Reference number: Jc6539; MUID:98172745; PMID:9511754
A:Accession: Jc6539
A:Molecule type: mRNA
A:Residues: 1-357 <M12>
A:Cross-references: DBJ:AB000509; NID:92982670; PIRN:BA25262.1; PID:92982671
C:Comment: This protein is involved in transduction of signals from various tumor necros
mphtoxin-beta receptor.
C:Genetics:
A:Map position: 1q32.3-1q41.1
C:Superfamily: CD40 receptor-associated protein CAP-1; RING finger homology
C:Keywords: coiled coil; tumor; zinc finger
F:41-90/Domain: RING finger homology <RNG>

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Query Match 39.6% Score 1192.5; DB 2; Length 557;
Best Local Similarity 42.0% Pred. No. 9,9e-62;
Matches 222; Conservative 121; Mismatches 178; Indels 21; Gaps 9;

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Oy 25 RSAGTPEVPEDEGGYKEKFKYKVEYKCEKCHLVLCSPKQTEGHRFCESCMALLS-S 83
      |||
Db 17 QNSGNSISLDFERSIEQVEFRLERKCAFCCHSVLHNPHTQCGHRFCCHLSRLRN 76
      |||
Oy 84 SSRKCTACOSIYKDKVFNCKCKRELAQITCRNESCAGQQLLGHILVHLKNDCH 143
      |||
Db 77 TVPCLPVDKENVISQVEFKDKCKRELVNLVYCSN-APCCNAKAVLIGRYQDHLQ-QCLF 134
      |||
Oy 144 EELPCVAPDCKEYLRKDLRDHYEAKCYREATCSHCKSGVPMIAQKHEDTDCPCVVVS 203
      |||
Db 135 QPVOCSNEKREPVLRDLDEHLSASQCFKCKCKKQVYVYINQNHENLCPREPVF 194
      |||
Oy 204 CPHKCVQTLRLSELNAHSECVNASTSCFKRYGCVFQSTNOQIKAHKSSAVQVNL 263
      |||
Db 195 CPNNCA-KILKTEVDHDLAVCEAEQDCPFKKYGCAYVTDKRRNLQNHESALREHRLV 253
      |||
Oy 264 KEMNSLSKFKVYLLQNSVESKNSIOSLHNOCSFEIEIRQKEMLRNNESKTLHLQRYL 323
      |||
Db 254 LEKVVQLEBQSLDKLSLEQKESIQQLAETIKLEKFEQFQRLPQKNSFLPNIQ-VF 312
      |||
Oy 324 DSQAEKLELDEKELRPF-----RQNNBEADSMKSSVESLQNNVTELESVDKSGAVAR 377
      |||
Db 313 ASHIDKSMLEAQVHQLQWNOQNKFDRLRLMEAVDIKOKITLLEND-----QR 365
      |||
Oy 378 TGLLESQLSRHDQMLSVHDIRLADMDLRFVLETAHYNGVLTWIRYKRRKQEAVMGK 437
      |||
Db 366 LAVLEETNKHDTIHINIKHQAQSKNEERFKLLBGTCTYNGKLIMKVDTYKMKKREAVDGH 425
      |||

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Oy 438 ISLYSOPFYNGFYKMCARVYLLGDGKGKTHLSFEFVIRGEYDALLPMPFKQKVTLM 497
      |||
Db 426 VSFISQSFYTSRQGYRLCARAYLLNGDSSGSGHLSLTFVIMRREFSILQMPFRQAVTLM 485
      |||
Oy 498 LMDQSSRRHLGDAFPDPPNSSFFKPTGEMNIAAGCPVEVAQVLEN--GTIKDDTIF 555
      |||
Db 486 LMDQ-SGKKNIMETFKPDPPNSSFFKPTGEMNIAAGCPVEVAQVLENKNAVYKDDTIF 544
      |||
Oy 556 IKVYVDTSLDLP 567
      |||
Db 545 LKVAVDLTLDLED 556
      |||

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RESULT 5

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I61512
TNF receptor associated factor 2 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 18-Aug-2000
C:Accession: I61512
R:Rothe, M.; Wong, S.C.; Henzel, W.J.; Goeddel, D.V.
Cell 78, 681-692, 1994
A:Title: A novel family of putative signal transducers associated with the cytoplasmic
A:Reference number: A54750; MUID:94349371; PMID:8069916
C:Accession: I61512
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-501 <R5>
A:Cross-references: GB:U35303; NID:9532620; PIRN:AAC37662.1; PID:9532621
C:Genetics:
A:Gene: TNFA2
C:Superfamily: CD40 receptor-associated protein CAP-1; RING finger homology
C:Keywords: zinc
F:30-78/Domain: RING finger homology <RNG>

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Query Match 27.8% Score 837.5; DB 2; Length 501;
Best Local Similarity 33.6% Pred. No. 3e-41;
Matches 196; Conservative 89; Mismatches 194; Indels 105; Gaps 17;

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Oy 3 SSKKNDSPGALQTNPLKLTDRSAGRPVPEDEGGYKEKFKVT-VEDKYKCEKCHLVLC 61
      |||
Db 2 AAAYTSQSLLELP-----GFSKTLGLTRLEKAKYLCSCAKNLR 42
      |||
Oy 62 SPKQTEGHRFCESCMALLSSSPKCTAC-----QEST--VKDKVFNCKCKRELA 112
      |||
Db 43 RPFQAGCHRCSPCLTSLTSGPNCAACYEGLEGISILSSSAFPDPAARRREVES 102
      |||
Oy 113 IQTYRNESRCAGDQTLTGHILVHLKNDCHFEELPCVAPDCKEYLRKDLRDHYEAKCY 172
      |||
Db 103 LPVCPND--GCTWKGTLKEYESCHGCLPFLTEC--PACKGLVRLSEKHNTEQDQPK 158
      |||
Oy 173 REATSHCKSGVPMIAQKHEDTDCPCVVVSCPHKCSVQTLRLSELNAHSECVNASTC 232
      |||
Db 159 KSLSCONCHRAPSHVDLEHYEV-CPKRPILC-DQCGKKIIRPREFQDHVNAAGSCRYLC 216
      |||
Oy 233 SPKRYGCVFQSTNOQIKAHKSSAVQVNLKEMNSLSLEKVS-----LLQNSV 282
      |||
Db 217 RETHVGCSEMYETENDLQHLRLREHLL--LSSFEAQSPQTLNQVBPBELLQRCQI 274
      |||
Oy 283 EKNKSIQSLHNOCSFEIEIRQKEMLRNNESKTLHLQRYDSQAEKLELDEKELRPF 342
      |||
Db 275 LEQK-LATFENTVCVLRNVER-----VAVTAECSSRHRDQD----- 312
      |||
Oy 343 NNEEADSMKSSVESLQNNVTELESVDKSGAVARNTGLLESQLSRHDQMLSVHDIRLAD 402
      |||
Db 313 -----KTEALSNNKQGLE-----RSIGL-----KDLAMADL 338
      |||
Oy 403 DLRFVLETAHYNGVLTWIRYKRRKQEAVMGKTLSTLSQPPYTGFGYKMCARVYLLNG 462
      |||
Db 339 EQKVESELYSTVDGFTWISDFTRRQDAVAGTRPALFSPFVTSRYGKMKCLVYLLNG 398
      |||
Oy 463 DQMGKTHLSFEFVIRGEYDALLPMPFKQKVTLMMDQSSRRHLGDAFPDPPNSSFFK 522
      |||

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Db 399 DGTGRGTHLSLFVVMKGPNDALLQWPNOKVTLMLLDH-NNREHVDAFRPDVTSFQ 457
 QY 523 KPTGEMNIASGCPVEVAQTULE-NGEYIKDDTFIKIYVTSDL 565
 Db 458 RPSVDNMIASGCPLEFVSKMEAKNKNSTYKDDALFIKAIYDLTGL 501

RESULT 6

556163
 tumor necrosis factor type 2 receptor associated protein - human

N:Alternate names: TNF receptor-associated protein

C:Species: Homo sapiens (man)

C>Date: 10-Oct-1995 #sequence_revision 01-Dec-1995 #text-change 03-Nov-2000

C:Accession: S56163; S58925; S58926; I38729

R:Song, H.Y.; Donner, D.B.

Biochem. J. 309, 825-829, 1995

A:Title: Association of a RING finger protein with the cytoplasmic domain of the human

A:Reference number: S56163; MUID:95366958; PMID:7639698

A:Accession: S56163

A:Molecule type: mRNA

A:Residues: 1-501 <SON1>

A:Cross-references: EMBL:U12597; NID:g975272

R:Song, H.Y.; Donner, D.

Submitted to the EMBL Data Library, July 1994

A:Description: Association of a RING finger protein with the cytoplasmic domain of the

A:Reference number: S58925

A:Accession: S58925

A:Molecule type: mRNA

A:Residues: 1-42,63-342,363-501 <SON2>

A:Cross-references: EMBL:U12597; NID:g975272

A:Accession: S58926

A:Molecule type: mRNA

A:Residues: 1-342, RPPQAGCGHRYCSFCLASIL', 363-501 <SON3>

A:Cross-references: EMBL:U12597; NID:g975272; PIDN:AAA87706.1; PID:g975273

R:Bothe, M.; Wong, S.C.; Henzel, W.J.; Goeddel, D.V.

Cell 78, 681-692, 1994

A:Title: A novel family of putative signal transducers associated with the cytoplasmic

A:Reference number: A54750; MUID:9449371; PMID:8069916

A:Accession: I38729

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-342, RPPQAGCGHRYCSFCLASIL', 363-501 <ROT>

A:Cross-references: EMBL:U12597; NID:g975272; PIDN:AAA87706.1; PID:g975273

C:Genetics:

A:Gene: GDB: TRAF2; TRAF

A:Cross-references: GDB:6268629; OMIM:601895

A:Map position: 9q34-q34

C:Superfamily: CD40 receptor-associated protein CAP-1; RING finger homology

C:Keywords: zinc finger

F:30-78/Domain: RING finger homology <RNG>

Query Match 27.0%; Score 811; DB 2; Length 501;
 Best Local Similarity 35.2%; Pred. No. 1e-39;

Matches 196; Conservative 86; Mismatches 177; Indels 98; Gaps 21;

QY 36 OGGYEKEFKYT-VEDEKYCEKHLYLCPKQTECHRRFCESMAALLSSSPKCTAC-OE 93
 Db 16 QGFSKTLTGTLKLEAKYLCASCRNLRPPQAGCGHRYCSFCLASILSSSPQNCACAYHE 75
 QY 94 STVKDNV-----FKDNCKRETLALQIYCRNESRGCALQTLGHLLVLLKNDCHHEE 145
 Db 76 GYIEGISTLSSSAFPNNAAREVESLPAVC--PSDCTMKGLTKER-----ESCHGR 128
 QY 146 LPCVR---PDCKEYLRKDLNDHVEKACKYREAFCSHCKSGVPMIALQKHEDTDCPCVVV 202
 Db 129 CPLMLTECPACKGLVRLGEKERHLEHECPERSLSCRHRCAPCCADYKAHNEV-CPKPL 187
 QY 203 SCPHKSGVOTLRLSELNAHLSECVNAPSTCSFKRYGCV--FQGNQDTKAHEASSAYOVH 260
 Db 188 TC-DGCGKKKIPREKFQDHYKTCGKRCVPCRFHAIGCLEVEGEEKO--EHEVOMLRHL 244
 QY 261 NLKEMWSLEKK-----VSLQN-ESVEKNSIOSLHQICSFEIEIRKREML 309

Db 245 AML--LSSVLEAKPPLGDSHAGSELLQCBSELEKKA--TFENTVYNREVER----- 295
 QY 310 RNNSEKILHLQRYDSQAELKEIDKEIRPFQNNWEADSMKSSVESLQNRTELESYDK 369
 Db 296 -----VAMTAACS-----RQHLDDO--KTEALSSKQOLE----- 325
 QY 370 SAGQVARNGLLESQLSRDMQLSVHDIRLMDIRFQVLETASTNGVLYMKIDYKRRK 429
 Db 326 -----RSIGL-----KDLAMADLEQVLEMEASTYDGVFIKISDFPKRL 365
 QY 430 QEAVNGKTLISYQEPYTGFGYKMCARVYVYNGDMGKTHLSLFFVIMRGEVALLPWP 489
 Db 366 QEAVAGRIPIRPSPAFYSRGYKMCALTYLNGDGTGTHLSLFFVVMKGPNDALLRMP 425
 QY 490 FKQKTYLMDGSSRRHLGDAFKDPPSSSKFKFTGEMNIASGCPVEVAQTULE-NGTY 548
 Db 426 FQKQTYLMLDD-NNREHVDAFRPDVTSFQRPVDNMIASGCPLEFVSKMEAKNSY 484
 QY 549 IKDDTFIKIYVTSDL 565
 Db 485 VRDDAIFIKAIYDLTGL 501

RESULT 7

55649
 TNFR-associated protein EB16 - human

C:Species: Homo sapiens (man)

C>Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text-change 08-Oct-1999

C:Accession: B55649

R:Mosialos, G.; Birkenbach, M.; Yalamanchili, R.; Vanarsdale, T.; Ware, C.; Kieff, E.

Cell 80, 389-399, 1995

A:Title: The Epstein-Barr virus transforming protein LMP1 engages signaling proteins

A:Reference number: A55649; MUID:95163092; PMID:7859281

A:Accession: B55649

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-416 <MOS>

A:Cross-references: GB:U19261; NID:g675461; PIDN:AAA62309.1; PID:g675462

Query Match 21.2%; Score 636.5; DB 2; Length 416;
 Best Local Similarity 35.3%; Pred. No. 1e-29;

Matches 164; Conservative 72; Mismatches 126; Indels 103; Gaps 17;

QY 138 KNDCHFEELPCVRPDCKEYLRKDLRHYEAKCYRATSTSHCKSGVPMIALQKHEDTDC 197
 Db 15 ENERPFGCPPTVCCDPKEP-----RALCCAGCLSENP-----RNGEDQIC 54
 QY 198 PCVYVSCPHKSGVOTL-----LRSELNAHLSECVNAPSTCSFKRYGCVFQGTNQDQIR 249
 Db 55 P-----KCRGDLQISISPGSRRLTQEKAN-PEVAEAGIGCPFAGVCGSPQSVQ 105
 QY 250 AHEASSAVOHNL-----KEMS-----NSLEKKVSLQ-NESVEKNNSTQ-SLH 292
 Db 106 EHEVTSQTSHTNLGCMQWKARLGGCLSGPMALEQNISDQLQAAVEVAGDLEVDY 165
 QY 293 NQICSFEIEIEROKEMLRNNESKILHLQRYIDSQAELKEIDKEIRPFQNNWEADSMK 352
 Db 166 RAPCS-----ESQDE-----LALQHPM--KELIALLEBKLVF-----E 198
 QY 353 SVESLQRYVELSSVNDKSAQOVARNGLLESQLSRH-----DOMTSVHDIRLA 400
 Db 199 NIVAVLNKEVE-----ASHLALATSIHQSDLRERITLSLQRYVELQOTLAQKQDALG 251
 QY 401 DMDIRFOVLETASTNGVLYIRDYKRRQEAAMGTSLISQPFYTGFGYKMCARVYL 460
 Db 252 KLEQSLRLMEASFDGTFMKLTITNVTRGHESACGTFVLEFPAFTYAYGKGLCLRLYL 311
 QY 461 NGDMGKTHLSLFFVIMRGEVALLPWPFKQKQVTLMLDQSSRRHLGDAFKPDPNSS 520
 Db 312 NGDGTGKRTHLSLFFVIMRGEVALLPWPFRKNVTFTMLDD-NNRHAIADARPDLSAS 370
 QY 521 FKPTGEMNIASGCPVEVAQTULEN--GYIKDDTFIKIYVTS 563

Db 371 FORPOSENNVAGSGLRFLPFLSLQSPKHAAYKDDTMFLKIVETS 415

RESULT 8

AS4750

TNF receptor associated factor 1 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999

C:Accession: AS4750

R:Roche, M.; Wong, S.C.; Henzel, W.J.; Goeddel, D.V.

Cell 78, 681-692, 1994

A:Title: A novel family of putative signal transducers associated with the cytoplasmic

A:Reference number: AS4750; MUID:4434937; PMID:8069916

A:Accession: AS4750

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-409 <RES>

A:Cross-references: GB:L35302; NID:g532618; PIDN:AAC37663.1; PID:g532619

C:Genetics:

A:Gene: TRAF1

Query Match

Best Local Similarity 36.6%; Score 628; DB 2; Length 409;

Matches 154; Conservative 69; Mismatches 128; Indels 70; Gaps 13;

173 REATCSHCKSQVPMALQKHEDTDCPCVYVSCPHKCSVQTLRLSELNHLSECVNAPSTC 232

Db 28 RVLCTACTLSE---NLNDDERDRCPCRADNLHPVSGSPLTGE-KVH-SDVAEALIMC 81

223 SFKRYGCVFGTNOQIKHAESSAVQHVNL-----LKEKNSNS-----LEKKVSL 277

Db 82 PFAGVGCSEFKSPQSMQHEATSOSSHLXLLAVLKEKSSPGSNLSAPALERNLSEL 141

278 QNESVEKKSQSLHNOICSEFEIEROKEMLRNNSKILHLQRYDSQAEK-LKEIDKE 336

Db 142 Q-----LQAAVEATGDELVDCYRAPCESQEBELQHLVH-----EKLLQLEEK 186

337 IRRPQNMNEADSMKSSVESLQNRTELESVDKSGAVARNTGLLESLSR----- 388

Db 187 LRVF-----ANTVAVALNKEVE-----ASHLALASIHOSLDREHLISLEOR 228

389 ---DOMLSVHDRLADMDLRFQVLETASYNGVLIMKIRYKRRKOAVMKTLSLQSP 444

Db 229 VVELDQTLAKQVQVGLKLEHSLRLMEASFDGTFLMKTITNTKRESHCRTVSLFSPA 288

445 FTTGFTGKMCARVLYLNDGDKGKTHLSLFEYINRGEVDALLPMPFKQVYVLMMDQSS 504

Db 289 FTTAKYGYKLCLRLYLNDGSGKTHLSLFEYINRGEVDALLPMPFKQVYVLMMDQ-NN 347

505 RRLHLDAPDPDNSSSPFKPTGEMINASGCPVFAQVLEEN--GTYIKDDTIFIKVYDT 562

Db 348 RERHLDARFDPDLSASFQRPQSETNVASGCLFPLSLQSPKHAAYVDDIMFLKIVDT 407

QY 563 S 563

Db 408 S 408

RESULT 9

MLN 62 protein - human

C:Species: Homo sapiens (man)

C:Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 02-Sep-2000

C:Accession: J38026; S60681

R:Tomasetto, C.; Regnier, C.H.; Moog-Lutz, C.; Mattel, M.G.; Chenard, M.P.; Lidereau, R.

Genomics 28, 367-376, 1995

A:Title: Identification of four novel human genes amplified and overexpressed in breast

A:Reference number: J37080; MUID:96039245; PMID:7490069

A:Accession: J38026

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-470 <RES>

A:Cross-references: EMBL:X80200; NID:g951276; PIDN:CAAS6491.1; PID:g951277

A:Note: submitted to the EMBL Data Library, July 1994

C:Genetics:

A:Gene: MLN62; CARL1

C:Superfamily: CD40 receptor-associated protein CAP-1; RING finger homology

F:14-63/Domain: RING finger homology <RRN>

Query Match 18.6%; Score 560.5; DB 2; Length 470;

Best Local Similarity 24.9%; Pred. No. 3e-25;

Matches 147; Conservative 75; Mismatches 173; Indels 195; Gaps 13;

38 GYKEKVTVEEDKYKCEKHLVLCSPKQ-TEGHRFCECMAALLSSSPKCTACQESIV 96

Db 3 GFDFKFLERPKRRLCLPLCGKPMREPVQVSTGCHRCDDTCLDFSEGVKCPEDQLPDK 62

97 KQVFEKNDCKRRLALQYICRNESSGCAEQLTGLHLYLNNDHFELPCVRPD-CKE 155

Db 63 YAKIYDPPELEVQVGLPLRCHISEGCMSSGRLNLOGLH-NTCSFNVIYC--FRRCM 119

156 KVLKDLRDHVEKACKYREATCSHCKSQVPMALQKH----- 193

Db 120 KLSRDLRALHLDHCPKRLKCEFCGCDPSGEAVESHEDMCQESYCEKNGARMRGL 179

194 -----DT-----DCCVYVSCPHKCSVQTLRLSELNHL 222

Db 180 LAQATSECPKRPQCTYCTKEEFPTIQSHOYQCPRLPVACPGVGTAVAREDLPGHL 239

223 SE-CVNAPTSCFKRYGCVFGTNOQIKHAESSAVQHVNLKEMNSLEKVSLLQNES 281

Db 240 KDSQNTALVLCPEKDSGCKHRCPKLMARHVESVYVPLHMM----- 281

282 VERKNSQSLHNOICSEFEIEROKEMLRNNSKILHLQRYDSQAEK-LKEIDKEIRPR 341

Db 282 -----CA-----LVSRQDELQELRREL----- 299

QY 342 QNNEADSMKSSVESLQNRTELESVDKSGAVARNTGLLESLSRNDMLSHDRLAD 401

Db 300 -----BELSV----- 304

QY 402 MDLRFQVLETASYNGVLIMKIRYKRRKOAVMKTLSLQSPFYTGFGYKMCARVLYN 461

Db 305 -----GSDGVILIMKISYGRRLDPAKAKKPNLECSPPAFYHNKYGKQVAFN 353

QY 462 GDGNGKTHLSLFEYINRGEVDALLPMPFKQVYVLMMDQ-----SSRRLGDAKRPDP 517

Db 354 GNGSGEGTHSLYIRVLPGFADNILEMPFARVTFSLDSDGLAKPKQHVETFFRPDP 413

QY 518 SSSPKR-----TGEMINASGCPVFAQVLENGTYIKDDTIFIKVYDT 561

Db 414 WKNEQKGTWRGSLDESSLGFGYKPTISHODIKRNVYRDVAVFIRAAVE 463

RESULT 10

probable interleukin 1 signal-transducing protein TRAF6 - human

C:Species: Homo sapiens (man)

C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 02-Sep-2000

C:Accession: S71821; S78550

R:Cao, Z.; Xiong, J.; Takeuchi, M.; Kurama, T.; Goeddel, D.V.

Nature 383, 443-446, 1996

A:Title: TRAF6 is a signal transducer for interleukin-1.

A:Reference number: S71821; MUID:96434892; PMID:8637778

A:Accession: S71821

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-522 <CAO>

A:Cross-references: EMBL:U08798; NID:g1732425; PIDN:AAB38751.1; PID:g1732426

R:Cao, Z.; Xiong, J.; Takeuchi, M.; Kurama, T.; Goeddel, D.V.

submitted to the EMBL Data Library, October 1996

A:Reference number: S78550

A:Accession: S78550

A:Molecule type: mRNA

A:Residues: 1-275, 'A', 277-522 <CAM>

A:Cross-references: EMBL:U08798; NID:g1732425; PIDN:AAB38751.1; PID:g1732426

QY 194 DTDCPCVVVSCPHKCSVOTLLRSELSEAHSECYNAPSTCSFKRYGCVFQGTNOOIKAAHEA 253
 DB 196 KT-CPMPIDSCGSCVKIERKSIIDHENDCCNTQIPCKYFEGGC----- 240
 QY 254 SSAVOHNLKEMNSLEKAVSLQNESVEKNSIOSLHNOICSELEIEROKEMLRNNE 313
 DB 241 -----KVEKRSSELQ----- 251
 QY 314 SKILHQRVIDSQAEKLELDKEIRPFRONWEADSKSSVESIQNRTELESVDKSAGO 373
 DB 252 -----HLEEV-----MHQNV-----NGILIEKLTQNV-----GQ 275
 QY 374 VARNTEGLLESOLSRHDD-----LSYHDIRLADMDIRFOYLETA-----SYNGVL-ITKIR 423
 DB 276 SKKT-----HDELTKKIEDLSLYIKFSDACKRKQVLPKALDICSNGYRKNKWIIS 325
 QY 424 DY-----KRRQEAVMGKTSLSYOPFTGYFGYKMCARVYLNDGKSGKTHLSLFPVI- 477
 DB 326 NYSSVANSKLNQALSSPMSLSLHLF-----QVC--YFPRKD--ENKEYISLYLRVN 374
 QY 478 -----MRGEYDALLPWPFRQKQVTLMLMDGSSRRHLGDAFKPDNSSSFKEKFTGEMNI 530
 DB 375 NIEPRNSLKEVYSFTL-----VNVLDKRSKITKED-----KKRVEFTSSE 414
 QY 531 ASGCPVFAQTVL--ENGTIKDITIFIKYIV 560
 DB 415 GWGKGFLLSDLINKENGMNSDKLLEIYI 446

RESULT 13

hypothetical protein T1217.7 [imported] - Arabidopsis thaliana
 B96692
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C:Accession: B96692
 R:Thelodopsis, A.; Ecker, J.R.; Palm, C.J.; Federpiet, N.A.; Kaul, S.; White, O.; Alonso,
 Chiu, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 Jensen, N.F.; Hughes, B.; Hultzer, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maltli, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: B96692
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-313 <STO>
 A:Cross-references: GB:AE005173; NID:g11054583; PIDN:ANG27858.1; GSPDB:GN00141
 C:Genetics:
 A:Gene: T1217.7
 A:Map position: 1

Query Match

Best Local Similarity 29.0%; Pred. NO. 0.0045;
 Matches 60; Conservative 23; Mismatches 93; Indels 31; Gaps 8;

QY 49 DRYKCEKHLVLCSP-KOTECGHRPCESCMAALLSSSSPKTACQESYVKDKVFQDNCK 107
 DB 40 DLDPCIPICHAULTSPFQCDNCHICSSCCTKLRN---KCPSCALPTGN--FRRIME 92
 QY 108 RETLALQIYCRNESGCAQLLGLHLVHLKNDCHFEELPCVRPOCKEVLKRDJRDH-- 165
 DB 93 RVEAVAVVCPVKKHGTCTKESYKELIHEK--DCRFALCYCAPKCNISGVYKDLYSHFY 151
 QY 166 VEKACRYRATSCSHCK-----SOVPMIALQKHEDTDCPCVVVSCPHKCSV 210
 DB 152 VNHVDTWNIIGGNGFAGWLRISSEKTLVQYGGPLIAVQCKREKQGVVTVNCTAPCAP 211
 QY 211 QTLNSELSEAHUS--ECVNAAPTSCSK 235

DB 212 GV---GELSELSYKMPKGNSTMMK 235

RESULT 14

149642
 estrogen-responsive finger protein - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
 C:Accession: 149642
 R:Orlino, A.; Inoue, S.; Ikeda, K.; Noji, S.; Muramatsu, M.
 J. Biol. Chem. 270, 24406-24413, 1995
 A:Title: Molecular cloning, structure, and expression of mouse estrogen-responsive fl
 A:Reference number: 149642; MUID:96025835; PMID:7592654
 A:Accession: 149642
 A:Status: Preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-634 <RES>
 A:Cross-references: GB:U63902; NID:g1088466; PIDN:BA009941.1; PID:g1088467
 C:Superfamily: RING finger homology
 C:Keywords: zinc
 F:9-59/Domain: RING finger homology <RNG>

Query Match

Best Local Similarity 18.7%; Pred. NO. 0.07;
 Matches 75; Conservative 69; Mismatches 130; Indels 128; Gaps 17;

QY 49 DRYKCEKHLVLCSPKOTECGHRPCESCMAALLSSSSP--KCTACQESI-VKDKVFKDN- 104
 DB 9 EELSCSVCELEKREPVTTPGHNFTSCDETWVVGPPRCPQCKKYQVPRLOLKNV 68
 QY 105 -CCRE-----ITALQIYCRNESGCAEOLTLGLVHLKN 139
 DB 69 MCNAVDEQLAEQARIPVDMPPARFSASATQVACDH---CLTEIAVKTCLVCMAS 124
 QY 140 DC-----HFEELPCVRPCKEVLKDLRDHKEK---KYREATCSHCKSQVPMIL 189
 DB 125 FCEHILRPHDS-----PARQDHLQSPIRDLLRRKCTOHNRLREFCP----- 168
 QY 190 QKHEDTDCPCVVVSCPHK-CSVOTLLRSELSEAHSECYNAPSTCSFKRYGCVFQGTNOOI 248
 DB 169 ---EHGICIHICLVEIKTSCPTTL--SQASADL----- 197
 QY 249 KAHBASAVOHNLKEMNSLEKAVSLQNESVEKNSIOSLHNOICSELEIEROKEM 308
 DB 198 -----EYKLRNKLTIMHSHNGATKALEDRSQOOCVQDSMKKMD 229
 QY 309 LRNESKTLHQRVID---SQAEKLELDKEI-----RFRONWEADSKSSVES 356
 DB 240 LR---QETMEKKAVIDAETSSLRKLEEKRYGKDTTYOVLVKKSKMOKLAEVL 296
 QY 357 LQNRTELESVDKSA--GOVARNTEGLLESOLSRHDMLSVH 395
 DB 297 IMDKGEFFLEKAKAKLOGESTKRVYIPKIDLD-HDLIMGIY 337

RESULT 15

A43906
 nuclear phosphoprotein knf7 - African clawed frog

C:Species: Xenopus laevis (African clawed frog)
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 11-Jan-2000
 C:Accession: A43906; S27947
 R:Reddy, B.A.; Kloc, M.; Ecklin, L.
 Dev. Biol. 148, 107-116, 1991
 A:Title: The cloning and characterization of a maternally expressed novel zinc finger
 A:Reference number: A43906; MUID:92038424; PMID:1936552
 A:Accession: A43906
 A:Molecule type: mRNA
 A:Residues: 1-609 <RED>
 A:Cross-references: EMBL:M63705; NID:g214914; PID:g214915
 A:Note: sequence extracted from NCBI backbone (NCBIN:64515, NCBIP:64520)
 C:Genetics:
 A:Gene: knf7
 C:Superfamily: Xenopus nuclear phosphoprotein knf7; RING finger homology

C:Keywords: DNA binding, nucleus, phosphoprotein, zinc finger
F:141-190/Domain: RING finger homology <RNG>

Query Match 5.1%; Score 152.5; DB 2; Length 609;
Best local similarity 20.7%; Pred. No. 0.16;

Matches 69; Conservative 41; Mismatches 109; Indels 115; Gaps 12;

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QY 49 DKYCKECHLVLCSPKQTECGHNFCECM-AALLSSSPKCTACQPSIVKDFKDNCK 107
   : : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 141 EELTCLCEVELFKDPYVACGHNFCSCIDKAMEGSSFACPECRSTIDRK----- 192
QY 108 REILAQITCRNBSRCADQLTLGHLVHLKNDCHFEELPCVRPDCKEVLKKDLRDHYE 167
   : : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 193 -----YTINRYLANIA-----KKAACTPVTVPVEKTRP-----LE 222
QY 168 KACKYREATCSHCKSQVPMIALQKHEDTDCPCVVVSCPHKCSVQTL-----RSEL 218
   : : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 223 KCEHDERLKLTK-----DDGTLSCVICRDSLKHASHNPLILDVAVGYREEL 271
QY 219 SAHLSECVNAPSTCSFKRYGCVFGTNOQIKAHEASSAVQHVNLKEMNSLEKKVSLIQ 278
   : : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 272 SA-----IVAPLEASLK-----VTEQLSSEQSDKTEQH----- 299
QY 279 NESVEKNKSIQSLHNOICFELIEIEROKEMLNNSKILHLQVIDSQAELKELDKETR 338
   : : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 300 -----NKNMSQYKEHITS---EFELKHLKFLREREKEL-----EQLKEQGENLL 340
QY 339 PFQON-----WEADSMKSSVESLQNRVTELESV 367
   : : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 341 TEMENNLVYMQESQDAIKKTIISLAKERMEDTDST 374

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Search completed: December 19, 2002, 14:55:59

Job time : 25 secs